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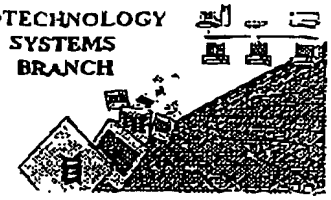
OIPE JC36 MAY 17 2004 PATENT & TRADEMARK OFFICE

BIOTECHNOLOGY SYSTEMS BRANCH



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/791,209
Source: EFW0
Date Processed by STIC: 3/10/04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 703-308-4212; FAX: 703-308-4221
***Effective 12/13/03*: TELEPHONE: 571-272-2510; FAX: 571-273-0221**

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>, EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to (**EFFECTIVE 12/01/03**): U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1D03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 10/08/03

Raw Sequence Listing Error Summary

ERROR DETECTED **SUGGESTED CORRECTION** SERIAL NUMBER: 10/791,209

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1____ Wrapped Nucleics / Wrapped Aminos — The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2____ Invalid Line Length — The rules require that a line not exceed 72 characters in length. This includes white spaces.

3____ Misaligned Amino Numbering — The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4____ Non-ASCII — The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5____ Variable Length — Sequence(s)____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6____ PatentIn 2.0 "bug" — A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7____ Skipped Sequences (OLD RULES) — Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence.
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8____ Skipped Sequences (NEW RULES) — Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9____ Use of n's or Xaa's (NEW RULES) — Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 ✓ Invalid <213> Response — Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11____ Use of <220> — Sequence(s) ____ missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 07/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12____ PatentIn 2.0 "bug" — Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13____ Misuse of n/Xaa — "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid

IFW0

RAW SEQUENCE LISTING DATE: 03/10/2004
PATENT APPLICATION: US/10/791,209 TIME: 16:44:32

Input Set : A:\SEQUENCE.ST25.txt
Output Set: N:\CRF4\03102004\J791209.raw

homo sapiens

3 <110> APPLICANT: Hahn, Soonkap
5 <120> TITLE OF INVENTION: DETECTION OF STRP, SUCH AS FRAGILE X SYNDROME
7 <130> FILE REFERENCE: 81671
:--> 9 <140> CURRENT APPLICATION NUMBER: US/10/791,209
:--> 9 <141> CURRENT FILING DATE: 2004-03-01
9 <160> NUMBER OF SEQ ID NOS: 6
11 <170> SOFTWARE: PatentIn version 3.2
13 <210> SEQ ID NO: 1
14 <211> LENGTH: 21
15 <212> TYPE: DNA
16 <213> ORGANISM: primer — Invalid Response, Mandatory, (PS.1) <213> Response has to be either Artificial/ Unknown or Genus Species.
18 <400> SEQUENCE: 1 ← Insert this response in section <223>
19 gtcaggcgct cagctccgtt t 21
22 <210> SEQ ID NO: 2
23 <211> LENGTH: 27
24 <212> TYPE: DNA
25 <213> ORGANISM: primer — Invalid response
27 <400> SEQUENCE: 2
28 ctcctccatc ttctcttcag ccctgct 27
31 <210> SEQ ID NO: 3
32 <211> LENGTH: 15
33 <212> TYPE: DNA
34 <213> ORGANISM: target sequence — Invalid Response
36 <400> SEQUENCE: 3
37 cgccgccgcc gccgc 15
40 <210> SEQ ID NO: 4
41 <211> LENGTH: 33
42 <212> TYPE: DNA
43 <213> ORGANISM: target sequence — Invalid Response
45 <400> SEQUENCE: 4
46 catcttctct tcagccctgc tagcgccggg agc 33
49 <210> SEQ ID NO: 5
50 <211> LENGTH: 33
51 <212> TYPE: DNA
52 <213> ORGANISM: probe — Invalid Response
54 <400> SEQUENCE: 5
55 gctcccggcg ctagcagggc tgaagagaag atg 33
58 <210> SEQ ID NO: 6
59 <211> LENGTH: 30
60 <212> TYPE: DNA
61 <213> ORGANISM: probe — Invalid Response
63 <400> SEQUENCE: 6
64 cggcggcggc ggcggcggcg gcggcggcgg 30

Does Not Comply
Corrected Diskette Needed

Please see item #10 on error summary sheet.

VERIFICATION SUMMARY DATE: 03/10/2004
PATENT APPLICATION: US/10/791,209 TIME: 16:44:33

Input Set : A:\SEQUENCE.ST25.txt
Output Set: N:\CRF4\03102004\J791209.raw

:9 M:270 C: Current Application Number differs, Replaced Current Application No
:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date